

### REMARKS

The Examiner rejected claims 1-4, 20, and 22-26, while withdrawing claims 5-19 and 21 from consideration. Claims 1-26 have been cancelled herein without prejudice. In addition, claims 27-58 have been added. Thus, claims 27-58 are pending.

The specification has been amended herein to insert sequence listing identifiers to correspond to the accompanying Sequence Listing.

Claims 27-42 recite a method for monitoring gene expression from virus infected cells within an organism, while claims 43-58 recite a Paramyxoviridae virus containing a nucleic acid sequence encoding a heterologous polypeptide. Support for these claims can be found throughout Applicants' specification and original claims. For example, page 9, lines 27-28 disclose that monitoring includes the process of determining the amount of gene expression occurring in an organism. See, also, the section extending from page 13, line 25 to page 14, line 2. Thus, no new matter has been added.

In light of the following remarks, Applicants respectfully request reconsideration and allowance of claims 27-58.

#### Rejections under 35 U.S.C. § 112, second paragraph

The Examiner rejected claims 4, 20, and 22-26 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 4, 20, and 22-26 have been cancelled herein without prejudice. Thus, this rejection is moot.

#### Rejections under 35 U.S.C. § 112, first paragraph

The Examiner rejected claims 1-4, 20, and 22-26 under 35 U.S.C. § 112, first paragraph, as containing subject matter which is not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Specifically, the Examiner stated that the "specification fails to provide adequate guidance and evidence for how the detection of a heterologous polypeptide in a biological fluid after administering a replication-competent Paramyxoviridae virus expressing

said heterologous polypeptide to a patient would be indicative of Paramyxoviridae growth in said patient and reduction in tumor size.”

Applicants respectfully disagree. A person having ordinary skill in the art at the time Applicants filed would have been able to make and use the originally claimed invention without undue experimentation. Claims 1-4, 20, and 22-26, however, have been cancelled herein. Thus, this rejection is moot.

Applicants' specification fully enables new claims 27-58. In fact, a person having ordinary skill in the art reading Applicants' specification would have been able to (1) make a Paramyxoviridae virus containing a nucleic acid sequence encoding a heterologous polypeptide and (2) administer that Paramyxoviridae virus to an organism. A person having ordinary skill in the art reading Applicants' specification also would have been able to (1) obtain biological fluid from that organism and (2) detect the amount of heterologous polypeptide in that biological fluid. Thus, claims 27-58 are fully enabled.

Rejections under 35 U.S.C. §§ 102(b) and 103(a)

The Examiner rejected claim 20 under 35 U.S.C. § 102(b) as anticipated by or, in the alternative, under 35 U.S.C. § 103(a) as obvious over Kim *et al.* (Molecular Medicine Today, 2(1):519-527, 1996). Specifically, the Examiner stated that

Kirn teaches that replication-competent viruses are used as selective cancer therapeutics and the specific viruses used include tumor-targeting herpes simples viruses, Newcastle disease viruses and adenoviruses. Infection of a tumor cell with a replicating virus can increase the sensitivity of the cell to killing by cytokines such as TNF-alpha and interferon alpha. Kirn also teaches that addition of cytokine gene, such IL-2, to replicating virus genome can increase tumor killing effect (e.g. abstract, box 2, p. 521).

Applicants respectfully disagree. Original claim 20 is not anticipated by, or obvious in light of, the Kim *et al.* reference. Claim 20, however, has been cancelled herein. Thus, these rejections are moot.

Applicant : Stephen James Russell et al.  
Serial No. : 09/667,947  
Filed : September 22, 2000  
Page : 18


Attorney's Docket No.: 07039-298001

### CONCLUSION

Applicants submit that claims 27-58 are in condition for allowance, which action is requested. The Examiner is invited to call the undersigned agent at the telephone number below if such will advance prosecution of this application. The Commissioner is authorized to charge any fees or credit any overpayments to Deposit Account No. 06-1050. Attached is a marked-up version of the changes being made by the current amendment

Respectfully submitted,

Date: December 12, 2002

  
J. Patrick Finn III, Ph.D.  
Reg. No. 44,109

Fish & Richardson P.C., P.A.  
60 South Sixth Street  
Suite 3300  
Minneapolis, MN 55402  
Telephone: (612) 335-5070  
Facsimile: (612) 288-9696

**Version with markings to show changes made**

**In the specification:**

The paragraph at page 20, line 11 has been replaced with the following amended paragraph:

--The specific sequence of amino acids in the protease cleavage site depends on the catalytic mechanism of the protease, which is defined by the nature of the functional group at the protease's active site, as discussed above. For example, trypsin hydrolyzes peptide bonds whose carbonyl function is donated by either a lysine or an arginine residue, regardless of the length or amino acid sequence of the polypeptide chain. Factor Xa, however, recognizes the specific sequence Ile-Glu-Gly-Arg (SEQ ID NO:1), but hydrolyzes peptide bonds between Arg-Thr and Arg-Ile. Thus, a protease cleavage site comprises at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more amino acids. Optionally, additional amino acids can be present at the N-terminus and/or C-terminus of the recognition site.--

The table at page 21, line 18 has been replaced with the following amended table:

Table 1. Properties Of Some Proteases Associated With Post-Translational Processing			
Protease	Subcellular Localization	Tissue Distribution	Cleavage Signal
Furin	Golgi	Ubiquitous	RXKR ( <u>SEQ ID NO:2</u> )
MMP-2	Golgi	tumor cells	PLGLWA ( <u>SEQ ID NO:3</u> )
MT1-MMP	plasma membrane	tumor cells	PLGLWA ( <u>SEQ ID NO:3</u> )
caspase-1	secretory pathway	Ubiquitous	YEVDGW ( <u>SEQ ID NO:4</u> )
caspase-2	secretory pathway		VDVADGW ( <u>SEQ ID NO:5</u> )
caspase-3	secretory pathway		VDQMDGW ( <u>SEQ ID NO:6</u> )
caspase-4	secretory pathway		LEVVDGW ( <u>SEQ ID NO:7</u> )
caspase-6	secretory pathway		VQVDGW ( <u>SEQ ID NO:8</u> )
caspase-7	secretory pathway		VDQVDGW ( <u>SEQ ID NO:9</u> )
alpha-secretase	secretory pathway	Ubiquitous	amyloid precursor protein (APP)
proprotein convertase (subtilisin/kexin isozyme SKI-1)	endoplasmic reticulum	Ubiquitous	brain neutrophilic growth factor precursor (RGLT) ( <u>SEQ ID NO:10</u> )
tumor associated tyrosin		tumor cells	
foot and mouth disease virus, protease 2A			NFDLLKLAGDVESNPGP ( <u>SEQ ID NO:11</u> )--

The paragraph at page 23, line 10 has been replaced with the following amended paragraph:

--An alternative to relying on cell-associated proteases is to use a sequence encoding a self-cleaving linker. In one embodiment of the invention, the foot and mouth disease virus (FMDV) 2A protease is used as linker. This is a short polypeptide of 17 amino acids that cleaves the polyprotein of FMDV at the 2A/2B junction. The sequence of the FMDV 2A propeptide is NFDLLKLAGDVESNPGP (SEQ ID NO:11). Cleavage occurs at the C-terminus of the peptide at the final glycine-proline amino acid pair and is independent of the presence of other FMDV sequences and cleaves even in the presence of heterologous sequences.--

The paragraph at page 30, line 8 has been replaced with the following amended paragraph:

--The H protein cytoplasmic tail comprises the amino-terminal 34 amino acids of the protein (sequence: NH<sub>2</sub>- MSPQRDRINAFYKDNPHPKGSRIVINREHLMIDR-COOH) (SEQ ID NO:12). Modification of H protein by removal of the 24 amino acids immediately following the initiator methionine (AA 2-25) results in a loss of fusogenic activity by the virus. In contrast, deletion of either 8 amino acids immediately following the initiator methionine (amino acids 2-9 deleted) or 14 amino acids between amino acids 2 and 17 (amino acids 3-16 deleted) enhance the fusogenic activity of the virus (Cathomen et al., 1998, J. Virol. 72:1224). These results indicate that membrane proximal amino acids 17 to 25 comprise a sequence necessary for fusion activity. The results also indicate that amino acids at least between those numbered 2 – 16 are involved in negative regulation of fusogenic activity. Therefore, in one embodiment, fusogenicity is enhanced by deletion of either amino acids 2-9, or 3-16. In a further embodiment of the invention, amino acids 2-16 are deleted. In still a further embodiment of the invention, amino acids 2-24 are deleted, and preferably 2-20. In one embodiment of the invention, the virus comprises a truncated H sequence comprising 8-14 fewer amino acids.--

The paragraph at page 31, line 2 has been replaced with the following amended paragraph:

--In one embodiment, the F protein is modified by alteration of its cytoplasmic tail, which comprises the carboxy-terminal 33 amino acids of the protein (sequence: NH<sub>2</sub>-RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL-COOH) (SEQ ID NO:13). Modifications of the F protein found to increase the fusogenic activity of the virus include addition of unrelated sequences to the C-terminus (for example, by alteration of the normal stop codon, or other means), and deletion of 16 or 24 C-terminal amino acids (Cathomen et al., 1998, J. Virol., supra). Viruses incorporating these changes include faster formation of syncytia, with a concomitant enhancement in the rate of cell killing. In another embodiment of the invention, a modified virus is provided which comprises a C-terminal tail comprising at least one deletion and/or substitution and which has enhanced fusogenic activity and/or cell killing effects. The addition or exchange of sequences have also been demonstrated to enhance the fusogenicity of the virus. Therefore, in a further embodiment of the invention, the F protein is modified by the addition of 28 amino acids, while in still a further embodiment, the C-terminal tail of the F protein is exchanged with the C-terminal tail of a Sendai virus.--

The paragraph at page 36, line 12 has been replaced with the following amended paragraph:

--The invention thus contemplates the introduction of selected cancer-associated protease cleavage sites into viruses. The cleavage of the F<sub>0</sub> precursor may be made dependent on a protease other than furin by replacement of the furin cleavage signal R-R-H-K-R (SEQ ID NO:14) at amino acids 108 to 112 of the measles virus (MV) or the corresponding residues of the other Paramyxoviridae viruses with that of another protease. Cleavage by furin occurs after arginine 112. Correct cleavage at this site is essential, because changing arginine 112 to leucine has been shown to result in aberrant cleavage and loss of fusion ability (Alkathib et al., 1994, J. Virol. 68:6770).--

The paragraph at page 37, line 23 has been replaced with the following amended paragraph:

--The F primer should have sequences complementary to the F<sub>0</sub> template sequence 3' of the nucleotides encoding the furin cleavage sequence (i.e., complementary to F<sub>1</sub> sequence

adjacent to the cleavage site), preceded by (i.e., 3' of) a randomized stretch of 12 bases corresponding in position to those encoding the furin cleavage site RHKR (SEQ ID NO:15). In order to avoid restoring furin cleavage, the "randomized" stretch of nucleotides should not be truly random, but rather be designed such that positions 1, 2 and 3 cannot be lysine or arginine (see Example 5).--

The paragraph at page 46, line 9 has been replaced with the following amended paragraph. Applicants note that the originally underlined text is double underlined below.

--To produce pCGHFurCP, primers Fur CP1.Nf and SfurinCP were used in a PCR reaction with pro-insulin template (ATCC) for 18 cycles at 94°C 1 min, 55°C 1 min and 72°C for 1 min. The resulting PCR fragment, tagged with Sfi-CP-Not was gel purified and digested with SfiI and NotI restriction enzymes. The pCGH backbond pCGH EGFr-was also digested with SfiI and NotI, and ligated with the prepared insert. Ligation reactions were transformed into competent *E. coli*, and resulting colonies screened by PCR for the presence of C-peptide insert. Successful transformants were grown to large scale and the DNA isolated.

FurCP1.Nf

ttt tcc ttt tgc ggc cgc ttt cat caa cgc ttc tgc agg gac ccc tc (SEQ ID NO:16)

SFurinCP

gtc cat gcg gcc cag ccg gcc CGA TTA AAG AGA gag gca gag gac ctg cag gtg gg

(SEQ ID NO:17)

V H A A Q P A R L K R E A E D L Q V (SEQ ID NO:18)--

The paragraph at page 47, line 1 has been replaced with the following amended paragraph. Applicants note that the originally underlined text is double underlined below.

--To produce pCGHG4SCP, primers G4SCP1.Nf and SG4SCP.b were used in a PCR reaction as described above.

G4SCP1.Nf

ttt tcc ttt tgc ggc cgc ttt cat cat caa cgc ttc tgc agg gac ccc tc (SEQ ID NO:19)

SG4SCP.b

gtc cat gcg gcc cag ccg gcc GGT GGA GGC GGT TCA gag gca gag gac ctg cag gtg gg

(SEQ ID NO:20)

V H A A Q P A G G G G S E A E D L Q V (SEQ ID NO:21)--

The paragraph at page 48, line 7 has been replaced with the following amended paragraph:

--F protein cytoplasmic tail mutations have been introduced to plasmids encoding full length measles virus genomic RNA (e.g., p(+)MV, Radecke et al., supra) as follows. Plasmids peFHLP, peFHLF and peFHLI (described in Schmid et al., 1992, Virology 188: 910) and plasmid peF (cSeV)HL were used as starting material for generation of full length measles virus plasmids encoding the following F mutants, respectively: mutant Fc+28, resulting from a stop codon mutation, comprises 28 amino acids of extraneous sequence appended to the C-terminus of the wild-type F protein (Fc+28 also has an additional Glu relative to the Edmonston B strain of the virus at position 27 relative to the transmembrane domain); mutant FcΔ16 lacks the 16 C-terminal amino acids of the F cytoplasmic tail (remaining sequence of the cytoplasmic tail is RGRCNKKGEQaGMSRPG (SEQ ID NO:22), where the lower case "a" also differs from the sequence of the Edmonston B strain of measles virus); mutant FcΔ24 lacks 24 C-terminal amino acids relative to the wild-type virus (remaining sequence of the cytoplasmic tail is RGRCNKKGE (SEQ ID NO:23)); and mutant FcSeV has the measles virus F protein cytoplasmic tail replaced by the F cytoplasmic tail from Sendai virus. Plasmid pcF (cSeV)HL was generated by subcloning a PstI –PacI PCR fragment encoding the SeV F cytoplasmic tail into peFHL. PCR was performed with pGem4-SVG<sub>0</sub> (described in Vidal et al., 1989, J. Virol. 63: 892) as the template and primers 5'-AAACTGCAGACTCAAAGGTCAATGC-3' (SEQ ID NO:24) and 5'-CCCTTAATTAATATACAGATCTCAACGGAT-3' (SEQ ID NO:25).--



The paragraph at page 49, line 10 has been replaced with the following amended paragraph:

--H protein mutant plasmids peHc $\Delta$ 8 (lacking amino-terminal amino acids 2-9), peHc $\Delta$ 14 (lacking amino terminal acids 3-16), and peHc $\Delta$ 24 (lacking amino-terminal amino acids 2-25) were constructed by subcloning a ClaI-EcoRI PCR fragment into peH5. peH5 is a shuttle vector for subcloning into the full-length p(+)MV (Cathomen et al., J. Virol., supra). peH5 contains a single ClaI site in the 5' untranslated region of the H protein and a single EcoRI site at the border between the transmembrane domain and the ectodomain, both sites introduced by silent mutations. PCR was performed with peH5 DNA as template and forward primers 5'-CCATCGATAATGGCCTTCTACAAAGATAACC-3' (peHc $\Delta$ 8) (SEQ ID NO:26), 5'-CCATCGATAATGAGCCATCCCAAGGGAAGTAGG-3' (peHc $\Delta$ 14) (SEQ ID NO:27), and 5'-CCATCGATAATGAACAGAGAACATCTTATGATT-3' (peHc $\Delta$ 24) (SEQ ID NO:28). The reverse primer annealed downstream of the H protein coding region in the plasmid.--

The paragraph at page 49, line 21 has been replaced with the following amended paragraph. Applicants note that the originally underlined text is double underlined below.

--To construct the H mutant in which the measles virus cytoplasmic tail was replaced with the Sendai virus H cytoplasmic tail, fusion PCR was performed. The SeV H-tail encoding region was amplified from the pGem4-SVHN plasmid template (described by Vidal et al., supra) with primers 5'-CCATCGATAATCATGGATGGTGATAGGGG-3' (SEQ ID NO:29) and 5'-GCAAAACATAAGGGGTGTCAACTTTACTTGA-3' (SEQ ID NO:30). The primer 5'-GACACCCCTTATGTTTTGCTGGC-3' (SEQ ID NO:31) and a primer annealing downstream of the region coding for the H transmembrane domain were used to amplify the MV H transmembrane encoding region. In the fusion step, the isolated PCR fragments with an overlapping sequence of 19 nucleotides (underline) were mixed and amplified with the external primers. The resulting fragment was digested with ClaI and EcoRI and then subcloned into peH5.--

The paragraph at page 52, line 4 has been replaced with the following amended paragraph:

--Measles virus F protein was modified by changing the arginine position 109 and the lysine at position 111 to asparagine. Cloning of the viral glycoprotein (H and F protein) genes into the expression vector pCG under the control of the CMV early promoter has been described by Cathomen et al., 1995, supra. The F cleavage mutant (pCG-Fcm) with substitutions in the furin recognition motif was prepared by introduction of site-specific mutations (underlined) with the complementary primers Fcm1 (5'-GCTTCAAGTAGGAACCACAACAGATTTGCGGG-3') (SEQ ID NO:32) and Fcm2 (5'-CCCGCAAATCTGTTGTGGTTCCTACTTGAAGC-3') (SEQ ID NO:33) into the double-stranded pCG-F plasmid using the QuikChange Site-Directed Mutagenesis Kit (Stratagene). After dideoxy sequencing of the complete F gene, the mutagenized plasmid was used for transfection of 293 and Vero cells.--

The paragraph at page 58, line 8 has been replaced with the following amended paragraph:

--In this example, the standard MV F cleavage signal RHKR (SEQ ID NO:15), recognised by furin, is mutated using random primers to generate a library with potentially novel cleavage specificities. To avoid restoring furin sensitivity, primers are designed such that positions 1,2,3, cannot be arginine or lysine.

	Furin Cleavage ▼						
	1	2	3	4	5	6	7
MV F0	R	H	K	R	F	A	G
	Furin sensitive site				Beginning of F1 polypeptide		

Arginine is coded by (single amino acid codes):

AGG  
AGA  
CGG  
CGA  
CGC  
CGT

Lysine is coded by:

AAG

AAA--

The paragraph at page 58, line 27 has been replaced with the following amended paragraph:

--The possible permutations of bases (as a result possible amino acids) are as shown:

Furin cleavage ▼

1	2	3	4	5	6	7	
R	H	K	R	F	A	G	} (SEQ ID NO:35)
				L	I	A	

Primer:

XAT	XAT	XAT	XXX	TTC	GCA	GGT	} (SEQ ID NO:36)--
XCC	XCC	XCC	XXX	TTA	ATA	GCT	
XTX	XTX	XTX	XXX				

The paragraph at page 60, line 4 has been replaced with the following amended paragraph:

--In one embodiment of the invention, the targeting specificity of an attenuated virus was altered by displaying a single chain antibody (ScFv) on the surface of the virus. In this embodiment, cDNAs coding for scFvs against a human lymphocyte differentiation antigens CD38 and CD52 were ligated into a full length infectious clone of MV-Edm (Figure 5). The genes were inserted as in-frame fusions linked to the C-terminal codon of the H glycoprotein through a linker sequence encoding an IEGR (single amino acid [coade] code) (SEQ ID NO:37) factor Xa protease cleavage signal. MV-Edm recombinant viruses were recovered from these constructs and were amplified in CD46 receptor-positive Vero cells in which they replicated as efficiently as unmodified MV-Edm. Correct expression of the scFV domains was confirmed on immunoblots of cell lysates of infected Vero cells, and probed with an antibody against the H glycoprotein (Figures 6A-D).--

The paragraph at page 63, line 4 has been replaced with the following amended paragraph:

--CDNAs encoding the three forms of the scAb were transferred to a pCH-H vector (17) containing a Factor Xa cleavage site 3' to the H ORF from retroviral expression vectors (J. Zhang, data not shown) using PCR amplification (primer sequences: 5'-GCGCGCTGGCCCAGGTG-3' (SEQ ID NO:38) and 5'-TGCGGCCGCCCCGTTTC-3' (SEQ ID NO:39), BssHII and NotI sites underlined). For detection purposes, an amino-terminal Flag tag (DYKDDDDK) (SEQ ID NO:40) was inserted downstream of the ATG start codon of each H construct. DNA sequencing confirmed the integrity of all constructs. The cDNA encoding HXL was transferred from the pCG construct into a molecular clone of MV-Edmonston, p(+)MV-Nse(18). Virus was rescued as previously described (19).--

The paragraph at page 70, line 15 has been replaced with the following amended paragraph:

--The parental plasmids pCG-F and pCG-H code for the F and H proteins of MV-Edmonston (9). Plasmids pCG-H/SfiI/NotI and pCG-H/XsfiI/NotI, the second including a factor Xa protease (FXa) cleavage signal before the SfiI/NotI cloning sites, were constructed and digested with SfiI and NotI to provide the backbone in which the coding regions for the displayed domains were inserted. The constructs pCG-H/hEGF, pCG-H/XhEGF, pCG-H/hIGF1 and pCG-H/XhIGF1 were made by transferring the SfiI/NotI hEGF and hIGF1 fragments from pEGF-GS1A1 (Peng, k.W., 1997, Thesis. University of Cambridge)) and pIGFNA1 (Chadwick, et al., J. Mol. Biol. 285:485-494), respectively, into SfiI/NotI-digested pCG-H/SfiI/NotI and pCG-H/XsfiI/NotI. The coding sequence of the linker region (IEGRAAQPAMA, one letter code) (SEQ ID NO:41) is 5'-ATCGAGGGAAGGGCGGCCAGCCGGCCATGGCC-3' (SEQ ID NO:42). The four constructs were tested to verify their functionality in cell fusion assays.--

The paragraph at page 70, line 26 has been replaced with the following amended paragraph:

--The PacI-SpeI fragments containing the hybrid H genes were corrected to comply to the rule of six (7/Calain, et al., J. Virol. 67:4822-4830, 1993)) by a PCR deleting one nucleotide

between the stop codon (underlined) and the SpeI site (*italics*), the final sequence being 5'-TAGTAACTAGT (SEQ ID NO:43). The fragments were then inserted into PacI-SpeI digested p(+)MV-Nse (Singh, et al., J. Virol. 73:4823-4828, 1999) encoding the MV Edmonston antigenome, yielding plasmids p(+)MV-H/hEGF, p(+)MV-H/XhEGF, p(+)MV-H/hIGF1 and p(+)MV-H/XhIGF1.--

The paragraph at page 71, line 19 has been replaced with the following amended paragraph:

--To introduce the SfiI/NotI cloning site at the C-terminus of the H sequence, thus enabling ligands to be inserted as SfiI/NotI fragments, oligonucleotides HXmabak (5'-CCG GGA AGA TGG AAC CAA TGC GGC CCA GCC GGC CTC AGG TTC AGC GGC CGC ATA GTA GA-3') (SEQ ID NO:44) and Hspefor (5'-CTA GTC TAC TAT GCG GCC GCT GAA CCT GAG GCC GGC TGG GCC GCA TTG GTT CCA TCT TC-3') (SEQ ID NO:45) were synthesised. When annealed, these two oligonucleotides form a DNA fragment with XmaI and SpeI cohesive ends which was ligated with XmaI/SpeI digested (pCG-H(SfiI-) backbone. The correct sequence of this construct, pCG-H-SfiI/NotI was verified by DNA sequencing.--

The paragraph at page 71, line 27 has been replaced with the following paragraph:

--To make the construct pCG-H-FX-SfiI/NotI, which includes a factor Xa protease (FX) cleavage signal before the SfiI/NotI cloning sites at the C-terminus of the MV H sequence, oligonucleotides HXmaFXbak (5'-CCG GGA AGA TGG AAC CAA TAT CGA GGG AAG GGC GGC CCA GCC GGC CTC AGG TTC AGC-3') (SEQ ID NO:46) and HNotFXfor (5'-GGC CGC TGA ACC TGA GGC CGG CTG GGC CGC CCT TCC CTC GAT ATT GGT TCC ATC TTC-3') (SEQ ID NO:47) were synthesised. When annealed, these two oligonucleotides form a DNA fragment with XmaI and NotI cohesive ends which was ligated with the XmaI/NotI digested pCG-H-SfiI/NotI backbone. The correct sequence of this construct was verified by DNA sequencing.--

The paragraph at page 75, line 1 has been replaced with the following amended paragraph:

--Plates were washed three times with 200 µl TBS and bound virus was detected by incubation with 100 µl of a rabbit anti-Hcterm specific antiserum diluted 1:100 in 1% blocking solution for 2 hours at 4°C . The Hcterm antiserum was raised in rabbits against a peptide corresponding to the 12 H-protein carboxy-terminal amino acids (NH<sub>2</sub>-CTVTREDGTNRR) (SEQ ID NO:48) linked to keyhole limpet hemocyanin through the naturally occurring cysteine (C). For detection, peroxidase-conjugated goat anti-rabbit IgG (Jackson Immuno Research, 111-035-003) diluted 1:5000 in 1% blocking solution was added for 1 hour at 4°C and after intense washing the color reaction was performed using the POD substrate from Boehringer Mannheim (1 363 727).--

The paragraph at page 76, line 3 has been replaced with the following amended paragraph:

--The human epidermal growth factor (hEGF, 53 amino acids) were used to generate a hybrid protein in which the hEGF coding region was fused in frame with the H coding region, but eliminating the last two arginine residues, to avoid the possibility of introducing an undesired furin cleavage site (H/hEGF, Fig. 14A, second line from bottom). A flexible linker region (AAQPAMA) (SEQ ID NO:49) was added between the domains to increase the probability of independent folding function. In another embodiment, the human insulin-like growth factor-1 (hIGF1, 70 amino acids) was fused to the H protein. A factor Xa protease cleavage site (IEGR; SEQ ID NO:37) was added before the linker region (H/XhEGF, Fig. 14A, second line from bottom). Hybrid H/hIGF1 and H/XhIGF1 proteins were constructed (Fig. 14A, bottom line). When the hybrid proteins were co-expressed with a MV F protein, H/hEGF and H/XhEGF retained the same level of fusogenicity as parental H, whereas fusogenicity of H/hIGF1 and H/XhIGF1 was reduced but remained clearly over background.--

In the claims:

Claims 1-26 have been cancelled.